

# Arnab Pain

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/3235966/arnab-pain-publications-by-citations.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

202  
papers

18,564  
citations

57  
h-index

135  
g-index

259  
ext. papers

22,107  
ext. citations

11.4  
avg, IF

5.76  
L-index

#	Paper	IF	Citations
202	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , <b>2002</b> , 419, 498-511	50.4	3336
201	A promoter-level mammalian expression atlas. <i>Nature</i> , <b>2014</b> , 507, 462-70	50.4	1301
200	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , <b>2005</b> , 438, 1151-6	50.4	1114
199	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . <i>Nature</i> , <b>2005</b> , 438, 1105-15	50.4	1094
198	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , <b>2005</b> , 435, 43-57	50.4	1042
197	A comprehensive survey of the <i>Plasmodium</i> life cycle by genomic, transcriptomic, and proteomic analyses. <i>Science</i> , <b>2005</b> , 307, 82-6	33.3	662
196	Analysis of the <i>Plasmodium falciparum</i> proteome by high-accuracy mass spectrometry. <i>Nature</i> , <b>2002</b> , 419, 537-42	50.4	538
195	<i>Plasmodium falciparum</i> -infected erythrocytes modulate the maturation of dendritic cells. <i>Nature</i> , <b>1999</b> , 400, 73-7	50.4	489
194	A robust SNP barcode for typing <i>Mycobacterium tuberculosis</i> complex strains. <i>Nature Communications</i> , <b>2014</b> , 5, 4812	17.4	355
193	The genome of the simian and human malaria parasite <i>Plasmodium knowlesi</i> . <i>Nature</i> , <b>2008</b> , 455, 799-803	50.4	289
192	New insights into the blood-stage transcriptome of <i>Plasmodium falciparum</i> using RNA-Seq. <i>Molecular Microbiology</i> , <b>2010</b> , 76, 12-24	4.1	283
191	Genome sequence of <i>Theileria parva</i> , a bovine pathogen that transforms lymphocytes. <i>Science</i> , <b>2005</b> , 309, 134-7	33.3	259
190	Genomic-scale prioritization of drug targets: the TDR Targets database. <i>Nature Reviews Drug Discovery</i> , <b>2008</b> , 7, 900-7	64.1	244
189	Two nonrecombining sympatric forms of the human malaria parasite <i>Plasmodium ovale</i> occur globally. <i>Journal of Infectious Diseases</i> , <b>2010</b> , 201, 1544-50	7	235
188	Genome of the host-cell transforming parasite <i>Theileria annulata</i> compared with <i>T. parva</i> . <i>Science</i> , <b>2005</b> , 309, 131-3	33.3	235
187	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , <b>2015</b> , 7, 51	14.4	234
186	Platelet-mediated clumping of <i>Plasmodium falciparum</i> -infected erythrocytes is a common adhesive phenotype and is associated with severe malaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2001</b> , 98, 1805-10	11.5	212

185	The systematic functional analysis of Plasmodium protein kinases identifies essential regulators of mosquito transmission. <i>Cell Host and Microbe</i> , <b>2010</b> , 8, 377-87	23.4	195
184	Emergence of Indigenous Artemisinin-Resistant Plasmodium falciparum in Africa. <i>New England Journal of Medicine</i> , <b>2017</b> , 376, 991-3	59.2	178
183	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , <b>2014</b> , 12, 86	7.3	174
182	Comparative genomics of the fungal pathogens <i>Candida dubliniensis</i> and <i>Candida albicans</i> . <i>Genome Research</i> , <b>2009</b> , 19, 2231-44	9.7	165
181	The lipopolysaccharide and beta-1,3-glucan binding protein gene is upregulated in white spot virus-infected shrimp ( <i>Penaeus stylirostris</i> ). <i>Journal of Virology</i> , <b>2002</b> , 76, 7140-9	6.6	164
180	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , <b>2018</b> , 50, 307-316	36.3	160
179	Genome variation and evolution of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , <b>2007</b> , 39, 120-5	36.3	159
178	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. <i>Genome Biology</i> , <b>2014</b> , 15, R43	18.3	155
177	Adaptation of the genetically tractable malaria pathogen <i>Plasmodium knowlesi</i> to continuous culture in human erythrocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 531-6	11.5	154
176	Comparative genomics of the apicomplexan parasites <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> : <i>Coccidia</i> differing in host range and transmission strategy. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002567	7.6	154
175	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>ELife</i> , <b>2015</b> , 4, e06974	8.9	138
174	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3-9 and 13. <i>Nature</i> , <b>2002</b> , 419, 527-31	50.4	127
173	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , <b>2014</b> , 24, 1676-85	9.7	121
172	<i>Plasmodium falciparum</i> var gene expression is modified by host immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 21801-6	11.5	111
171	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. <i>Nature Communications</i> , <b>2014</b> , 5, 4754	17.4	107
170	Essential Role of the ESX-5 Secretion System in Outer Membrane Permeability of Pathogenic <i>Mycobacteria</i> . <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005190	6	105
169	iSCAN: An RT-LAMP-coupled CRISPR-Cas12 module for rapid, sensitive detection of SARS-CoV-2. <i>Virus Research</i> , <b>2020</b> , 288, 198129	6.4	102
168	A non-sense mutation in Cd36 gene is associated with protection from severe malaria. <i>Lancet, The</i> , <b>2001</b> , 357, 1502-3	40	89

167	A barcode of organellar genome polymorphisms identifies the geographic origin of Plasmodium falciparum strains. <i>Nature Communications</i> , <b>2014</b> , 5, 4052	17.4	83
166	Outcomes, infectiousness, and transmission dynamics of patients with extensively drug-resistant tuberculosis and home-discharged patients with programmatically incurable tuberculosis: a prospective cohort study. <i>Lancet Respiratory Medicine</i> , <b>2017</b> , 5, 269-281	35.1	80
165	Rapid single-molecule detection of COVID-19 and MERS antigens via nanobody-functionalized organic electrochemical transistors. <i>Nature Biomedical Engineering</i> , <b>2021</b> , 5, 666-677	19	78
164	Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. <i>BMC Medicine</i> , <b>2016</b> , 14, 31	11.4	77
163	A promoter polymorphism in the gene encoding interleukin-12 p40 (IL12B) is associated with mortality from cerebral malaria and with reduced nitric oxide production. <i>Genes and Immunity</i> , <b>2002</b> , 3, 414-8	4.4	76
162	Mutations in ppe38 block PE_PGRS secretion and increase virulence of Mycobacterium tuberculosis. <i>Nature Microbiology</i> , <b>2018</b> , 3, 181-188	26.6	74
161	Alteration of host cell phenotype by Theileria annulata and Theileria parva: mining for manipulators in the parasite genomes. <i>International Journal for Parasitology</i> , <b>2006</b> , 36, 9-21	4.3	73
160	Genome-wide discovery and verification of novel structured RNAs in Plasmodium falciparum. <i>Genome Research</i> , <b>2008</b> , 18, 281-92	9.7	72
159	Genome-wide functional analysis of Plasmodium protein phosphatases reveals key regulators of parasite development and differentiation. <i>Cell Host and Microbe</i> , <b>2014</b> , 16, 128-40	23.4	71
158	Functional characterization of the Plasmodium falciparum and P. berghei homologues of macrophage migration inhibitory factor. <i>Infection and Immunity</i> , <b>2007</b> , 75, 1116-28	3.7	69
157	A scalable pipeline for highly effective genetic modification of a malaria parasite. <i>Nature Methods</i> , <b>2011</b> , 8, 1078-82	21.6	68
156	The evolutionary dynamics of variant antigen genes in Babesia reveal a history of genomic innovation underlying host-parasite interaction. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 7113-31	20.1	66
155	The normal cellular prion protein is strongly expressed by myeloid dendritic cells. <i>Blood</i> , <b>2001</b> , 98, 3733-8.2	8.2	65
154	PolyTB: a genomic variation map for Mycobacterium tuberculosis. <i>Tuberculosis</i> , <b>2014</b> , 94, 346-54	2.6	64
153	Transition of Plasmodium sporozoites into liver stage-like forms is regulated by the RNA binding protein Pumilio. <i>PLoS Pathogens</i> , <b>2011</b> , 7, e1002046	7.6	64
152	Population genomics reveals that an anthropophilic population of Aedes aegypti mosquitoes in West Africa recently gave rise to American and Asian populations of this major disease vector. <i>BMC Biology</i> , <b>2017</b> , 15, 16	7.3	62
151	Population genomic structure and adaptation in the zoonotic malaria parasite Plasmodium knowlesi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 13027-32	11.5	62
150	Divergent mitochondrial respiratory chains in phototrophic relatives of apicomplexan parasites. <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 1115-31	8.3	62

149	A Comprehensive Subcellular Atlas of the Toxoplasma Proteome via hyperLOPIT Provides Spatial Context for Protein Functions. <i>Cell Host and Microbe</i> , <b>2020</b> , 28, 752-766.e9	23.4	61
148	Endosymbiosis undone by stepwise elimination of the plastid in a parasitic dinoflagellate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 5767-72	11.5	60
147	Re-evaluating the green versus red signal in eukaryotes with secondary plastid of red algal origin. <i>Genome Biology and Evolution</i> , <b>2012</b> , 4, 626-35	3.9	58
146	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. <i>Scientific Reports</i> , <b>2015</b> , 5, 15443	4.9	57
145	Genome-wide RIP-Chip analysis of translational repressor-bound mRNAs in the Plasmodium gametocyte. <i>Genome Biology</i> , <b>2014</b> , 15, 493	18.3	57
144	Experimental evolution, genetic analysis and genome re-sequencing reveal the mutation conferring artemisinin resistance in an isogenic lineage of malaria parasites. <i>BMC Genomics</i> , <b>2010</b> , 11, 499	4.5	56
143	Identification of the genes involved in odorant reception and detection in the palm weevil <i>Rhynchophorus ferrugineus</i> , an important quarantine pest, by antennal transcriptome analysis. <i>BMC Genomics</i> , <b>2016</b> , 17, 69	4.5	55
142	Differential var gene expression in the organs of patients dying of falciparum malaria. <i>Molecular Microbiology</i> , <b>2007</b> , 65, 959-67	4.1	54
141	Autoagglutination of malaria-infected red blood cells and malaria severity. <i>Lancet, The</i> , <b>2000</b> , 355, 1427-30	4.0	51
140	SARS-CoV-2 S1 and N-based serological assays reveal rapid seroconversion and induction of specific antibody response in COVID-19 patients. <i>Scientific Reports</i> , <b>2020</b> , 10, 16561	4.9	51
139	Identification of a novel conjugative plasmid in mycobacteria that requires both type IV and type VII secretion. <i>MBio</i> , <b>2014</b> , 5, e01744-14	7.8	50
138	Insight into the genome of <i>Aspergillus fumigatus</i> : analysis of a 922 kb region encompassing the nitrate assimilation gene cluster. <i>Fungal Genetics and Biology</i> , <b>2004</b> , 41, 443-53	3.9	50
137	Comparative genome analysis of three eukaryotic parasites with differing abilities to transform leukocytes reveals key mediators of Theileria-induced leukocyte transformation. <i>MBio</i> , <b>2012</b> , 3, e00204-12	7.8	48
136	Split photosystem protein, linear-mapping topology, and growth of structural complexity in the plastid genome of <i>Chromera velia</i> . <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 2447-62	8.3	47
135	Unraveling <i>Mycobacterium tuberculosis</i> genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. <i>BMC Genomics</i> , <b>2014</b> , 15, 991	4.5	45
134	Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, <i>Hypothenemus hampei</i> . <i>Scientific Reports</i> , <b>2015</b> , 5, 12525	4.9	44
133	Genome-wide transposon mutagenesis indicates that <i>Mycobacterium marinum</i> customizes its virulence mechanisms for survival and replication in different hosts. <i>Infection and Immunity</i> , <b>2015</b> , 83, 1778-88	3.7	44
132	READSCAN: a fast and scalable pathogen discovery program with accurate genome relative abundance estimation. <i>Bioinformatics</i> , <b>2013</b> , 29, 391-2	7.2	44

131	Genome-scale comparison of expanded gene families in <i>Plasmodium ovale wallikeri</i> and <i>Plasmodium ovale curtisi</i> with <i>Plasmodium malariae</i> and with other <i>Plasmodium</i> species. <i>International Journal for Parasitology</i> , <b>2016</b> , 46, 685-96	4.3	43
130	Recombination in <i>pe/ppe</i> genes contributes to genetic variation in <i>Mycobacterium tuberculosis</i> lineages. <i>BMC Genomics</i> , <b>2016</b> , 17, 151	4.5	43
129	<i>Plasmodium</i> P-Type Cyclin CYC3 Modulates Endomitotic Growth during Oocyst Development in Mosquitoes. <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1005273	7.6	42
128	Recombinations in staphylococcal cassette chromosome <i>mec</i> elements compromise the molecular detection of methicillin resistance in <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , <b>2014</b> , 9, e101419	3.7	42
127	Whole genome sequencing based characterization of extensively drug-resistant <i>Mycobacterium tuberculosis</i> isolates from Pakistan. <i>PLoS ONE</i> , <b>2015</b> , 10, e0117771	3.7	41
126	Normocyte-binding protein required for human erythrocyte invasion by the zoonotic malaria parasite <i>Plasmodium knowlesi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 7231-6	11.5	40
125	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. <i>Nature Methods</i> , <b>2020</b> , 17, 481-494	21.6	39
124	Proteomes and transcriptomes of the Apicomplexa--where's the message?. <i>International Journal for Parasitology</i> , <b>2009</b> , 39, 135-43	4.3	37
123	The rhoptry proteome of <i>Eimeria tenella</i> sporozoites. <i>International Journal for Parasitology</i> , <b>2013</b> , 43, 181-8	4.3	36
122	Spontaneous duplication of a 661 bp element within a two-component sensor regulator gene causes phenotypic switching in colonies of <i>Pseudomonas tolaasii</i> , cause of brown blotch disease of mushrooms. <i>Molecular Microbiology</i> , <b>1997</b> , 25, 211-8	4.1	36
121	Comparative genomics of the Rab protein family in Apicomplexan parasites. <i>Microbes and Infection</i> , <b>2008</b> , 10, 462-70	9.3	36
120	<i>Plasmodium falciparum</i> antigenic variation: relationships between in vivo selection, acquired antibody response, and disease severity. <i>Journal of Infectious Diseases</i> , <b>2005</b> , 192, 1119-26	7	35
119	Expression analysis of the <i>Theileria parva</i> subtelomere-encoded variable secreted protein gene family. <i>PLoS ONE</i> , <b>2009</b> , 4, e4839	3.7	35
118	Timing of host feeding drives rhythms in parasite replication. <i>PLoS Pathogens</i> , <b>2018</b> , 14, e1006900	7.6	35
117	Whole genome sequence analysis of <i>Mycobacterium suricattae</i> . <i>Tuberculosis</i> , <b>2015</b> , 95, 682-688	2.6	34
116	Assembly of the genome of the disease vector <i>Aedes aegypti</i> onto a genetic linkage map allows mapping of genes affecting disease transmission. <i>PLoS Neglected Tropical Diseases</i> , <b>2014</b> , 8, e2652	4.8	34
115	Host-directed editing of the SARS-CoV-2 genome. <i>Biochemical and Biophysical Research Communications</i> , <b>2021</b> , 538, 35-39	3.4	34
114	A genetic barcode of SARS-CoV-2 for monitoring global distribution of different clades during the COVID-19 pandemic. <i>International Journal of Infectious Diseases</i> , <b>2020</b> , 100, 216-223	10.5	33

113	Candidate Essential Genes in Burkholderia cenocepacia J2315 Identified by Genome-Wide TraDIS. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1288	5.7	32
112	Genome-wide mutagenesis and multi-drug resistance in American trypanosomes induced by the front-line drug benznidazole. <i>Scientific Reports</i> , <b>2017</b> , 7, 14407	4.9	31
111	A selenocysteine tRNA and SECIS element in Plasmodium falciparum. <i>Rna</i> , <b>2005</b> , 11, 119-22	5.8	31
110	Genes involved in sex pheromone biosynthesis of Ephestia cautella, an important food storage pest, are determined by transcriptome sequencing. <i>BMC Genomics</i> , <b>2015</b> , 16, 532	4.5	29
109	Recruitment of EB1, a master regulator of microtubule dynamics, to the surface of the Theileria annulata schizont. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003346	7.6	29
108	Highly diverged novel subunit composition of apicomplexan F-type ATP synthase identified from Toxoplasma gondii. <i>PLoS Biology</i> , <b>2018</b> , 16, e2006128	9.7	28
107	Light harvesting complexes of Chromera velia, photosynthetic relative of apicomplexan parasites. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , <b>2013</b> , 1827, 723-9	4.6	28
106	Analysis of the role of recA in phenotypic switching of Pseudomonas tolaasii. <i>Journal of Bacteriology</i> , <b>2000</b> , 182, 6532-5	3.5	27
105	Diversity of extracellular proteins during the transition from the 'proto-apicomplexan' alveolates to the apicomplexan obligate parasites. <i>Parasitology</i> , <b>2016</b> , 143, 1-17	2.7	26
104	Exome and transcriptome sequencing of Aedes aegypti identifies a locus that confers resistance to Brugia malayi and alters the immune response. <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1004765	7.6	25
103	Comprehensive evaluation of Toxoplasma gondii VEG and Neospora caninum LIV genomes with tachyzoite stage transcriptome and proteome defines novel transcript features. <i>PLoS ONE</i> , <b>2015</b> , 10, e0124473	3.7	25
102	Functional Pangenome Analysis Shows Key Features of E Protein Are Preserved in SARS and SARS-CoV-2. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2020</b> , 10, 405	5.9	25
101	Progenitor strain introduction of Mycobacterium bovis at the wildlife-livestock interface can lead to clonal expansion of the disease in a single ecosystem. <i>Infection, Genetics and Evolution</i> , <b>2017</b> , 51, 235-238	4.5	24
100	Malaria parasites regulate intra-erythrocytic development duration via serpentine receptor 10 to coordinate with host rhythms. <i>Nature Communications</i> , <b>2020</b> , 11, 2763	17.4	23
99	Enteric Infections Circulating during Hajj Seasons, 2011-2013. <i>Emerging Infectious Diseases</i> , <b>2017</b> , 23,	10.2	23
98	Metabolic pathway redundancy within the apicomplexan-dinoflagellate radiation argues against an ancient chromalveolate plastid. <i>Communicative and Integrative Biology</i> , <b>2016</b> , 9, e1116653	1.7	22
97	Defining the protein interaction network of human malaria parasite Plasmodium falciparum. <i>Genomics</i> , <b>2012</b> , 99, 69-75	4.3	22
96	Early Humoral Response Correlates with Disease Severity and Outcomes in COVID-19 Patients. <i>Viruses</i> , <b>2020</b> , 12,	6.2	21

95	The population structure of <i>Vibrio cholerae</i> from the Chandigarh Region of Northern India. <i>PLoS Neglected Tropical Diseases</i> , <b>2014</b> , 8, e2981	4.8	20
94	New Initiatives for Management of Red Palm Weevil Threats to Historical Arabian Date Palms*. <i>Florida Entomologist</i> , <b>2011</b> , 94, 733-736	1	20
93	Long- and short-term selective forces on malaria parasite genomes. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001099	6	20
92	Characterization and gene expression analysis of the <i>cir</i> multi-gene family of <i>Plasmodium chabaudi</i> <i>chabaudi</i> (AS). <i>BMC Genomics</i> , <b>2012</b> , 13, 125	4.5	19
91	Microfibrinous silver-coated polymeric scaffolds with tunable mechanical properties. <i>RSC Advances</i> , <b>2017</b> , 7, 34331-34338	3.7	17
90	A divergent cyclin/cyclin-dependent kinase complex controls the atypical replication of a malaria parasite during gametogony and transmission. <i>ELife</i> , <b>2020</b> , 9,	8.9	17
89	A Poisson hierarchical modelling approach to detecting copy number variation in sequence coverage data. <i>BMC Genomics</i> , <b>2013</b> , 14, 128	4.5	16
88	PhyTB: Phylogenetic tree visualisation and sample positioning for <i>M. tuberculosis</i> . <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 155	3.6	16
87	Proteogenomic Investigation of Strain Variation in Clinical <i>Mycobacterium tuberculosis</i> Isolates. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 3841-3851	5.6	15
86	A multiple genome analysis of <i>Mycobacterium tuberculosis</i> reveals specific novel genes and mutations associated with pyrazinamide resistance. <i>BMC Genomics</i> , <b>2017</b> , 18, 769	4.5	15
85	Global transcriptome profiling and functional analysis reveal that tissue-specific constitutive overexpression of cytochrome P450s confers tolerance to imidacloprid in palm weevils in date palm fields. <i>BMC Genomics</i> , <b>2019</b> , 20, 440	4.5	14
84	The draft genome of <i>Mycobacterium aurum</i> , a potential model organism for investigating drugs against <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium leprae</i> . <i>International Journal of Mycobacteriology</i> , <b>2015</b> , 4, 207-16	0.9	14
83	Rapid identification of genes controlling virulence and immunity in malaria parasites. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006447	7.6	14
82	Accelerating Early Antituberculosis Drug Discovery by Creating <i>Mycobacterial</i> Indicator Strains That Predict Mode of Action. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	14
81	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing <i>Mycobacterium tuberculosis</i> genetic diversity in Portuguese-speaking countries. <i>Infection, Genetics and Evolution</i> , <b>2019</b> , 72, 44-58	4.5	14
80	Analysis of nuclear and organellar genomes of <i>Plasmodium knowlesi</i> in humans reveals ancient population structure and recent recombination among host-specific subpopulations. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1007008	6	13
79	Translational repression of the <i>cpw-wpc</i> gene family in the malaria parasite <i>Plasmodium</i> . <i>Parasitology International</i> , <b>2016</b> , 65, 463-71	2.1	13
78	Whole genome sequencing of amplified <i>Plasmodium knowlesi</i> DNA from unprocessed blood reveals genetic exchange events between Malaysian Peninsular and Borneo subpopulations. <i>Scientific Reports</i> , <b>2019</b> , 9, 9873	4.9	13



77	Plasmodium kinesin-8X associates with mitotic spindles and is essential for oocyst development during parasite proliferation and transmission. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1008048	7.6	13
76	A reference genome and methylome for the Plasmodium knowlesi A1-H.1 line. <i>International Journal for Parasitology</i> , <b>2018</b> , 48, 191-196	4.3	12
75	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical Salmonella enterica Serovar Senftenberg Variant in China. <i>Journal of Clinical Microbiology</i> , <b>2016</b> , 54, 2014-22	9.7	12
74	Targeted disruption of py235ebp-1: invasion of erythrocytes by Plasmodium yoelii using an alternative Py235 erythrocyte binding protein. <i>PLoS Pathogens</i> , <b>2011</b> , 7, e1001288	7.6	12
73	The genomic variation landscape of globally-circulating clades of SARS-CoV-2 defines a genetic barcoding scheme		12
72	Multidrug-Resistant Mycobacterium tuberculosis of the Latin American Mediterranean Lineage, Wrongly Identified as Mycobacterium pinnipedii (Spoligotype International Type 863 [SIT863]), Causing Active Tuberculosis in South Brazil. <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 3805-11	9.7	11
71	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. <i>BMC Medicine</i> , <b>2020</b> , 18, 24	11.4	10
70	Complete genome sequence of Mycobacterium phlei type strain RIVM601174. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 3284-5	3.5	10
69	Pheromone receptor of the globally invasive quarantine pest of the palm tree, the red palm weevil (Rhynchophorus ferrugineus). <i>Molecular Ecology</i> , <b>2021</b> , 30, 2025-2039	5.7	10
68	Proteomic profiling of the plasma of Gambian children with cerebral malaria. <i>Malaria Journal</i> , <b>2018</b> , 17, 337	3.6	10
67	Integrated transcriptomic and proteomic analysis of pathogenic mycobacteria and their esx-1 mutants reveal secretion-dependent regulation of ESX-1 substrates and WhiB6 as a transcriptional regulator. <i>PLoS ONE</i> , <b>2019</b> , 14, e0211003	3.7	9
66	Discovering, Characterizing, and Applying Acyl Homoserine Lactone-Quenching Enzymes to Mitigate Microbe-Associated Problems Under Saline Conditions. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 823	5.7	9
65	SnoopCGH: software for visualizing comparative genomic hybridization data. <i>Bioinformatics</i> , <b>2009</b> , 25, 2732-3	7.2	9
64	miR-126-5p by direct targeting of JNK-interacting protein-2 (JIP-2) plays a key role in Theileria-infected macrophage virulence. <i>PLoS Pathogens</i> , <b>2018</b> , 14, e1006942	7.6	9
63	A subcellular atlas of Toxoplasma reveals the functional context of the proteome		9
62	Proteomic Investigation of Rhizoctonia solani AG 4 Identifies Secretome and Mycelial Proteins with Roles in Plant Cell Wall Degradation and Virulence. <i>Journal of Agricultural and Food Chemistry</i> , <b>2016</b> , 64, 3101-10	5.7	9
61	Short sequence motif dynamics in the SARS-CoV-2 genome suggest a role for cytosine deamination in CpG reduction. <i>Journal of Molecular Cell Biology</i> , <b>2021</b> , 13, 225-227	6.3	9
60	Emergence of multidrug-resistant of the Beijing lineage in Portugal and Guinea-Bissau: a snapshot of moving clones by whole-genome sequencing. <i>Emerging Microbes and Infections</i> , <b>2020</b> , 9, 1342-1353	18.9	8

59	Genetic Determinants Associated With Survival of in the Model. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1118	5.7	8
58	Comparative Genomic and Transcriptomic Analyses of Subtypes Provide New Insights Into Their Pathogenicity and Taxonomy. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2020</b> , 10, 122	5.9	7
57	Whole genome sequencing provides additional insights into recurrent tuberculosis classified as endogenous reactivation by IS6110 DNA fingerprinting. <i>Infection, Genetics and Evolution</i> , <b>2019</b> , 75, 103948	4.5	7
56	Complete genome sequence of <i>Mycobacterium vaccae</i> type strain ATCC 25954. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 6339-40	3.5	7
55	Simultaneous detection and mutation surveillance of SARS-CoV-2 and multiple respiratory viruses by rapid field-deployable sequencing. <i>Med</i> , <b>2021</b> , 2, 689-700.e4	31.7	7
54	First report of harboring in Saudi Arabia. <i>Antimicrobial Resistance and Infection Control</i> , <b>2019</b> , 8, 203	6.2	7
53	Draft Genome Sequences of <i>Pseudomonas fluorescens</i> BS2 and <i>Pusillimonas noertemannii</i> BS8, Soil Bacteria That Cooperate To Degrade the Poly- $\epsilon$ -Glutamic Acid Anthrax Capsule. <i>Genome Announcements</i> , <b>2013</b> , 1,		6
52	A Robust, Safe, and Scalable Magnetic Nanoparticle Workflow for RNA Extraction of Pathogens from Clinical and Wastewater Samples. <i>Global Challenges</i> , <b>2021</b> , 5, 2000068	4.3	6
51	The genome of the zoonotic malaria parasite <i>Plasmodium simium</i> reveals adaptations to host switching. <i>BMC Biology</i> , <b>2021</b> , 19, 219	7.3	6
50	A fast and cost-effective microsampling protocol incorporating reduced animal usage for time-series transcriptomics in rodent malaria parasites. <i>Malaria Journal</i> , <b>2019</b> , 18, 26	3.6	5
49	A proportion of mutations fixed in the genomes of in vitro selected isogenic drug-resistant <i>Mycobacterium tuberculosis</i> mutants can be detected as minority variants in the parent culture. <i>FEMS Microbiology Letters</i> , <b>2015</b> , 362, 1-7	2.9	5
48	Influx of diverse, drug resistant and transmissible <i>Plasmodium falciparum</i> into a malaria-free setting in Qatar. <i>BMC Infectious Diseases</i> , <b>2020</b> , 20, 413	4	5
47	<i>Theileria</i> parasites subvert E2F signaling to stimulate leukocyte proliferation. <i>Scientific Reports</i> , <b>2020</b> , 10, 3982	4.9	5
46	Turkish and Japanese <i>Mycobacterium tuberculosis</i> sublineages share a remote common ancestor. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 45, 461-473	4.5	5
45	Complete genome sequence of <i>Mycobacterium fortuitum</i> subsp. <i>fortuitum</i> type strain DSM46621. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 6337-8	3.5	5
44	The Lipopolysaccharide and $\beta$ ,3-Glucan Binding Protein Gene Is Upregulated in White Spot Virus-Infected Shrimp ( <i>Penaeus stylirostris</i> ). <i>Journal of Virology</i> , <b>2002</b> , 76, 8978-8978	6.6	5
43	The genome of the zoonotic malaria parasite <i>Plasmodium simium</i> reveals adaptations to host-switching		5
42	Novel tumour suppressor roles for GZMA and RASGRP1 in <i>Theileria annulata</i> -transformed macrophages and human B lymphoma cells. <i>Cellular Microbiology</i> , <b>2020</b> , 22, e13255	3.9	5

41	Saudi Arabian SARS-CoV-2 genomes implicate a mutant Nucleocapsid protein in modulating host interactions and increased viral load in COVID-19 patients		5
40	Theileria highjacks JNK2 into a complex with the macroschizont GPI (GlycosylPhosphatidylinositol)-anchored surface protein p104. <i>Cellular Microbiology</i> , <b>2019</b> , 21, e12973	3.9	5
39	Unity in diversity: lessons from Candida. <i>Nature Reviews Microbiology</i> , <b>2009</b> , 7, 763	22.2	4
38	SARS-CoV-2 genomes from Saudi Arabia implicate nucleocapsid mutations in host response and increased viral load.. <i>Nature Communications</i> , <b>2022</b> , 13, 601	17.4	4
37	Functional pangenome analysis suggests inhibition of the protein E as a readily available therapy for COVID-2019		4
36	Antennal transcriptome sequencing and identification of candidate chemoreceptor proteins from an invasive pest, the American palm weevil, <i>Rhynchophorus palmarum</i> . <i>Scientific Reports</i> , <b>2021</b> , 11, 8334	4.9	4
35	Protein phosphatase 1 regulates atypical mitotic and meiotic division in Plasmodium sexual stages. <i>Communications Biology</i> , <b>2021</b> , 4, 760	6.7	4
34	Understanding the antifouling mechanisms related to copper oxide and zinc oxide nanoparticles in anaerobic membrane bioreactors. <i>Environmental Science: Nano</i> , <b>2019</b> , 6, 3467-3479	7.1	4
33	Metagenomics of Imported Multidrug-Resistant Mycobacterium leprae, Saudi Arabia, 2017. <i>Emerging Infectious Diseases</i> , <b>2020</b> , 26, 615-617	10.2	3
32	SVAMP: sequence variation analysis, maps and phylogeny. <i>Bioinformatics</i> , <b>2014</b> , 30, 2227-9	7.2	3
31	Genome Sequences of the Oxytetracycline Production Strain Streptomyces rimosus R6-500 and Two Mutants with Chromosomal Rearrangements. <i>Genome Announcements</i> , <b>2014</b> , 2,		3
30	Complete genome sequence of Mycobacterium xenopi type strain RIVM700367. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 3282-3	3.5	3
29	Hot and sexy moulds!. <i>Nature Reviews Microbiology</i> , <b>2006</b> , 4, 244-5	22.2	3
28	Proteomic profiling of the brain of mice with experimental cerebral malaria. <i>Journal of Proteomics</i> , <b>2018</b> , 180, 61-69	3.9	3
27	Global mapping of protein subcellular location in apicomplexans: the parasite as we've never seen it before. <i>Access Microbiology</i> , <b>2019</b> , 1,	1	3
26	Pheromone receptor of the globally invasive quarantine pest of the palm tree, the red palm weevil ( <i>Rhynchophorus ferrugineus</i> )		3
25	Performance of Commercially Available Rapid Serological Assays for the Detection of SARS-CoV-2 Antibodies. <i>Pathogens</i> , <b>2020</b> , 9,	4.5	3
24	Plasmodium Kinesin-8X associates with mitotic spindles and is essential for oocyst development during parasite proliferation and transmission		2

23	iSCAN: An RT-LAMP-coupled CRISPR-Cas12 module for rapid, sensitive detection of SARS-CoV-2		2
22	Short sequence motif dynamics in the SARS-CoV-2 genome suggest a role for cytosine deamination in CpG reduction <b>2021</b> ,		2
21	Early Humoral Response Correlates with Disease Severity and Outcomes in COVID-19 Patients		2
20	Dynamics and within-host interaction of <i>Theileria lestoquardi</i> and <i>T. ovis</i> among naive sheep in Oman. <i>Scientific Reports</i> , <b>2020</b> , 10, 19802	4.9	2
19	Quick and Easy Assembly of a One-Step qRT-PCR Kit for COVID-19 Diagnostics Using In-House Enzymes. <i>ACS Omega</i> , <b>2021</b> , 6, 7374-7386	3.9	2
18	Genome Sequence of a Multidrug-Resistant Strain of <i>Stenotrophomonas maltophilia</i> with Carbapenem Resistance, Isolated from King Abdullah Medical City, Makkah, Saudi Arabia. <i>Genome Announcements</i> , <b>2015</b> , 3,		1
17	Sequence data swell for nematodes. <i>Nature Reviews Microbiology</i> , <b>2008</b> , 6, 800-1	22.2	1
16	Strength in diversity. <i>Nature Reviews Microbiology</i> , <b>2004</b> , 2, 358-9	22.2	1
15	Simultaneous Detection and Mutation Surveillance of SARS-CoV-2 and co-infections of multiple respiratory viruses by Rapid field-deployable sequencing		1
14	Disruption of the coordination between host circadian rhythms and malaria parasite development alters the duration of the intraerythrocytic cycle		1
13	Identification of gene fusion events in that encode chimeric proteins. <i>NAR Genomics and Bioinformatics</i> , <b>2020</b> , 2, lqaa033	3.7	1
12	<i>Plasmodium vinckei</i> genomes provide insights into the pan-genome and evolution of rodent malaria parasites. <i>BMC Biology</i> , <b>2021</b> , 19, 69	7.3	1
11	Insights into the ancestry evolution of the complex from analysis of. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab070	3.7	1
10	Meningococcal carriage among Hajj pilgrims, risk factors for carriage and records of vaccination: a study of pilgrims to Mecca. <i>Tropical Medicine and International Health</i> , <b>2021</b> , 26, 453-461	2.3	1
9	Protein Phosphatase 1 regulates atypical mitotic and meiotic division in <i>Plasmodium</i> sexual stages		1
8	The Genetics of Resistance to Malaria <b>2004</b> , 479-500		1
7	Pangenome Analysis of the Soilborne Fungal Phytopathogen and Development of a Comprehensive Web Resource: RsolaniDB.. <i>Frontiers in Microbiology</i> , <b>2022</b> , 13, 839524	5.7	1
6	Global research alliance in infectious disease: a collaborative effort to combat infectious diseases through dissemination of portable sequencing.. <i>BMC Research Notes</i> , <b>2022</b> , 15, 44	2.3	0

- 5 Whole-genome sequencing as a tool for studying the microevolution of drug-resistant serial Mycobacterium tuberculosis isolates. *Tuberculosis*, **2021**, 131, 102137 2.6 ○
- 4 Development of the Myzozoan Aquatic Parasite Perkinsus marinus as A Versatile Experimental Genetic Model Organism. *Protist*, **2021**, 172, 125830 2.5 ○
- 3 Molecular pathogenesis of malaria **2019**, 193-206
- 2 Fungi behaving badly. *Nature Reviews Microbiology*, **2005**, 3, 832-3 22.2
- 1 Crohn's Disease Patient Infected With Multiple Co-occurring Nontuberculous Mycobacteria. *Inflammatory Bowel Diseases*, **2020**, 26, e65-e67 4.5